MicrobesOnline: A Community Resource for Data-Integrated Comparative Functional Genomics (R-009)

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http://vimss.lbl.gov/

INTRODUCTION

Since 2003, the MicrobesOnline.org web site of the Environmental Stress Pathway Project (ESPP) has provided novel web-based tools for comparative genomics of prokaryotes.

- •To describe the potential functions of genes, MicrobesOnline includes protein family analyses (from InterPro and COG), metabolic maps (from KEGG), and links to characterized genes (from UniProt).
- *To examine each gene's evolutionary history, MicrobesOnline includes precomputed phylogenetic trees for all the gene families, and displays them with the genes' genomic context, or it compares the gene tree to the species tree.
- Users can also compute their own sequence alignments and phylogenetic trees. *To examine the potential regulation of genes of interest, MicrobesOnline also includes tools for finding sequence motifs and for finding regulatory sites.
- •MicrobesOnline includes microarray data: it shows up-regulated or downregulated genes or operons, shows changes in expression patterns in a metabolic map, or gives an overview of the expression pattern for specific genes of interest. •Finally, users can use our gene annotation interface to add or revise gene names, descriptions, EC or GO assignments, or comments.

Currently MicrobesOnline hosts over 350 public genomes and 20 private genomes, and ~300 public and private microarrays. Our web site is unique in that, in addition to providing our own automated analyses, it allows users to perform their own analyses of genes of their choice.

All of these tools are freely available at our web site:

MicrobesOnline



Our examples concern perR and related genes in Desulfovibrio vulgaris Hildenborough. Searching for perR (above) returns search results (below) where there are links to view the various pages relating

Search results for perR in Desulfovibrio vulgaris Hildenborough

	From Synonym: 1 found	Add all genes to cart				
	Genes					
1	GODHSTB VMSS208612 Per	R DVU3095.0RF04117 323738	4 - 3237770	-) Desulfovibrio v	ulgaris Hildenborough	Adi

COG735. Fe2+/Zn2+ uptake regulation proteins linorganic ion transport and metabolism.

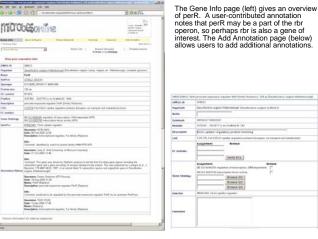
Every gene page has links for viewing basic gene annotatations, operon predictions, domain alignments from InterPro, BLASTp homologs, and the public annotation interface.

Future Work

- More links to external databases/web sites, such as RegTransDB. EcoCyc, IMG, STRING, PhIGs
- •More microarray data, and a new interface including heat maps
- Protein-protein interaction data Metabolomic and proteomic data
- Operon-wise significance analysis of microarray data



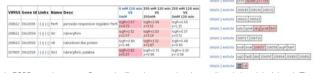
Gene Information and Annotation Pages



VMSS Predicted Operon

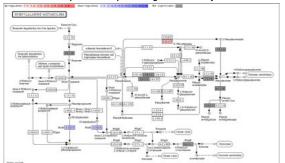
The operon view of rbr (left) shows that perR is not predicted by our methods to be part of the rbr operon. User contributed annotations allow for manually-entered information to supplement

Microarray Data Display and Analysis

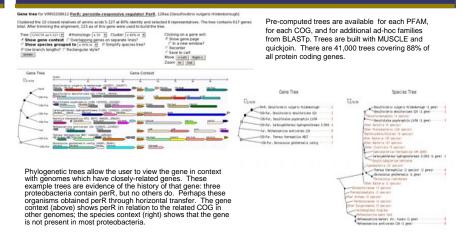


In ESPP experiments, perR was significantly up-regulated, as well as rbr2 and rbr (above). The operon view of this microarray experiment (upper right) shows that rbr was up-regulated, as was

Example KEGG map with integrated Microarray data



Phylogenetic Tree Browser



Gene Cart Workbench Tools

Gene Cart Multiple Sequence Alignments Cart Summary / Cart: ASM Cart #1 / Generale MSA



Phylogenetic Tree Creation



Motif Search : MEME / Weeder / AlignAce



Genome Browser



ACKNOWLEDGEMENT

ESPP is part of the Virtual Institute for Microbial Stress and Survival supported by the U. S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomics Program: GTL through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U. S. Department of Energy.

Website:

http://www.microbesonline.org